

Appl. No. : 10/648,848
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AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

LISTING OF CLAIMS

1-23. (Canceled)

24. (Previously presented) A method of determining the location of a decoding sequence on an array composition, said method comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation distributed on said discrete sites, wherein each subpopulation comprises identifier nucleic acid sequences comprising:

1) the same primer sequence; and

2) a different decoding sequence adjacent to said primer sequence;

wherein said microspheres are distributed on said surface; and

b) providing a first set of combinatorial decoding probes comprising a priming sequence complementary to said primer sequence, a variable sequence, and at least one decoding nucleotide included in said variable sequence that will basepair with at least one nucleotide of at least one of said decoding sequences, wherein said first set comprises different subsets of combinatorial decoding probes, each subset having the same decoding nucleotide and a first label specific to said same decoding nucleotide; and

c) adding to said array composition a subset of said first set of combinatorial decoding probes and detecting the presence of said first label, thereby determining the location of said decoding sequence on said array composition.

25. (Previously presented) The method according to claim 24, further comprising:

d) providing a second set of combinatorial decoding probes comprising said priming sequence complementary to said primer sequence, said variable sequence and at least one decoding nucleotide included in said variable sequence that will basepair with at least one nucleotide of at least one of said decoding sequences at a position that is

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different from the position that basepairs with said decoding nucleotide of said first set of combinatorial decoding probes, wherein said second set comprises different subsets of combinatorial decoding probes, each subset having the same decoding nucleotide and a second label specific to said same decoding nucleotide; and

e) adding to said array composition a subset of said second set of combinatorial decoding probes and detecting the presence of said second label.

26. (Canceled)

27. (Previously presented) The method of claim 25, wherein said population of microspheres is randomly distributed on said discrete sites.

28. (Previously presented) The method of claim 25, wherein said identifier nucleic acid sequence comprises genomic DNA.

29. (Previously presented) The method of claim 25, wherein said identifier nucleic acid sequence is prepared by an amplification technique.

30. (Previously presented) The method of claim 25, wherein said first set of combinatorial decoding probes comprises four subsets.

31. (Previously presented) The method of claim 25, wherein nucleotides in said variable sequence comprise universal bases.

32. (Currently amended) The method of claim 25, wherein at each variable sequence nucleotide position, all possible naturally occurring nucleotides are represented in at least one ~~nucleic acid~~ decoding sequence of said subset ~~first set of decoding sequences~~.

33. (Currently amended) The method of claim 25, wherein said decoding nucleotide ~~comprises is~~ an internal nucleotide of said variable sequence.

34. (Currently amended) The method of claim 25, wherein said decoding nucleotide ~~comprises is~~ a terminal nucleotide of said variable sequence.

35. (Previously presented) A method of determining the location of a decoding sequence on an array surface, said method comprising:

a) providing at least a first and a second subpopulation of identifier nucleic acid sequences distributed on said surface, said identifier nucleic acid sequences comprising the same primer sequence and a different decoding sequence adjacent to said primer sequence;

b) providing a first set of combinatorial decoding probes comprising a priming sequence complementary to said primer sequence, a variable sequence and at least one decoding nucleotide included in said variable sequence that will basepair with at least one nucleotide of at least one of said decoding sequences, wherein said first set comprises different subsets of combinatorial decoding probes, each subset having the same decoding nucleotide; and

c) adding to said array composition a subset of said first set of combinatorial decoding probes and determining the location of said decoding sequence on said array composition.

36. (Previously presented) The method according to claim 35, further comprising:

d) providing a second set of combinatorial decoding probes comprising said priming sequence complementary to said primer sequence, said variable sequence and at least one decoding nucleotide included in said variable sequence that will basepair with at least one nucleotide of at least one of said decoding sequences at a position that is different from the position that basepairs with said decoding nucleotide of said first set of combinatorial decoding probes, wherein said second set comprises different subsets of combinatorial decoding probes, each subset having the same decoding nucleotide; and

e) adding to said array composition a subset of said second set of combinatorial decoding probes.

37. (Previously presented) The method of claim 36, wherein said identifier nucleic acid sequence comprises genomic DNA.

38. (Previously presented) The method of claim 36, wherein said identifier nucleic acid sequence is prepared by an amplification technique.

39. (Previously presented) The method of claim 36, wherein said first set of combinatorial decoding probes comprises four subsets.

40. (Previously presented) The method of claim 36, wherein nucleotides in said variable sequence comprise universal bases.

41. (Currently amended) The method of claim 36, wherein at each variable sequence nucleotide position, all possible naturally occurring nucleotides are represented in at least one nucleic acid decoding sequence of said ~~subset~~ first set of decoding sequences.

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42. (Currently amended) The method of claim 36, wherein said decoding nucleotide ~~comprises~~ is an internal nucleotide of said variable sequence.

43. (Currently amended) The method of claim 36, wherein said decoding nucleotide ~~comprises~~ is a terminal nucleotide of said variable sequence.

44. (New) The method of claim 25, wherein at each variable sequence nucleotide position, all possible naturally occurring nucleotides are represented in at least one decoding sequence of said second set of decoding sequences.

45. (New) The method of claim 36, wherein at each variable sequence nucleotide position, all possible naturally occurring nucleotides are represented in at least one decoding sequence of said second set of decoding sequences.